Suggisters: 1) Please consent Sequerce Rules for valid format.

2) FII: all S. Oppheatrers filed on a after fluty!, 1998,

2) FII: all S. Oppheatrers filed on a after fluty!, 1998,

Let in new Sequerce Rules format.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/242,657

DATE: 02/09/2000
TIME: 09:53:45

INPUT SET: S34681.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

```
SEQUENCE LISTING
            GENERAL INFORMATION
                                                                     Does Not Comply
                                     use upper-case letters Corrected Diskette Needed
            General Information):
                                                all response must be on same live or heading
                   STREET: Gaerdesmuttevej
13
                    CITY: Hoersholm
14
15
                    COUNTRY: Denmark
                     POSTAL CODE (ZIP): DK-2970
17
         (ii) TITLE OF INVENTION: Artificial promoter libraries for
18
     selected
19
                   1 move we
                  organisms and promoters derived from such libraries
20
21
22
        (iii) NUMBER OF SEQUENCES: 58
                                            (IV) CORAKS PONDENCE ADORESS section

gols above

utible

OOS/MS-DOS

Lease #1.0, Version #1.30

Section
23
24
      ( √) (<del>f</del> v) COMPUTER READABLE FORM:
                (A) MEDIUM TYPE: Floppy disk
25
                (B) COMPUTER: IBM PC compatible
26
                (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27
                (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29
     (EPO)
      (IV) (V) CORRESPONDENCE ADDRESS:
(2(A)AOORFSSEE: Stanislaus Aksman
                Hunton & Williams
34 (B) STREET:
                1900 K Street, NW
35 (c) (17y:
                Washington, DC (20006-1109
36 (E) COUNTY; USA PROPE; (202) 955-1500
               Facsimile:
38 (F) 21P:1
                             (202) 778-2201
                                                           (ix) TELE COMMUNICATION INFORMATION:
         (vi) CURRENT APPLICATION DATA:
39
40
                (A) APPLICATION NUMBER: To Be Assigned
                (B) FILING DATE IN THE US PTO: February 19, 1999
41
                (C) ATTORNEY DOCKET-NO.: 55411.000002
42
                                                              ) goes under
                    REFERENCE / DOCKET NUMBER 1
43
         (vii) PRIOR APPLICATION DATA:
44
                                                                (Viii) ATTORNEY/ALENT INFORMATION:
                (A) APPLICATION NUMBER: DK 886/96
45
```

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DATE: 02/09/2000 TIME: 09:53:46

INPUT SET: S34681.raw

```
46 (B) FILING DATE: 23-AUG-1996
--> 47 (A) (C) PET APPLICATION NUMBER: PCT/DK97/00342
48 (B) FILING DATE: August 25, 1997
49
```

ERRORED SEQUENCES FOLLOW:

```
50
            (2) INFORMATION FOR SEQ ID NO: 1:
       51
       52
                  (i) SEQUENCE CHARACTERISTICS:
-->
       53
                       (A) LENGTH: 100 base pairs
       54
                       (B) TYPE: nucleic acid
       55
                       (C) STRANDEDNESS: double
                       (D) TOPOLOGY: linear
       56
       57
                 (ii) MOLECULE TYPE: DNA (genomic)
       58
       59
                (iii) HYPOTHETICAL: YES
       60
       61
       62
                (iv) ANTI-SENSE: NO
       63
                 (vi) ORIGINAL SOURCE:
       64
                       (A) ORGANISM: Lactococcus lactis
       65
       66
       67
                 (ix) FEATURE:
       68
                       (A) NAME/KEY: promoter
       69
                       (B) LOCATION: 26..82
       70
                       (C) IDENTIFICATION METHOD: experimental
       71
                       (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
       72
                              /standard_name= "Artificial promoter library"
       73
                              /note= "A degenerated sequence specifying a
       74
            mixture of
       75
                              artificial promoters covering a wide range of
            expression in
       77
                              small steps in L. lactis"
       78
       79
                 (ix) FEATURE:
       80
                       (A) NAME/KEY: misc feature
                       (B) LOCATION: 31..45
       81
       82
                       (D) OTHER INFORMATION:/standard name= "Consensus
       83
                              sequence"
       84
       85
                 (ix) FEATURE:
                       (A) NAME/KEY: misc feature
       86
       87
                       (B) LOCATION: 60..69
       88
                       (D) OTHER INFORMATION:/standard_name= "Consensus
       89
                              sequence"
       90
       91
                (ix) FEATURE:
                       (A) NAME/KEY: misc_feature
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```
(B) LOCATION: 74..82
 93
 94
                 (D) OTHER INFORMATION:/standard_name= "Consensus
 95
                        sequence"
 96
 97
           (ix) FEATURE:
 98
                 (A) NAME/KEY: -35 signal
 99
                 (B) LOCATION: 40..45
                 (D) OTHER INFORMATION:/standard name= "-35 box"
100
101
102
           (ix) FEATURE:
                 (A) NAME/KEY: -10 signal
103
104
                 (B) LOCATION: 63..68
105
                 (D) OTHER INFORMATION:/standard name= "Pribnow box"
106
107
           (ix) FEATURE:
                 (A) NAME/KEY: misc recomb
108
                 (B) LOCATION:3..25
109
                 (C) IDENTIFICATION METHOD: experimental
110
111
                 (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
112
                        /standard name= "Multiple cloning site"
113
                        /label= MCS .
114
                        /note= "A sequence specifying recognition sites
115
      for the
                        restriction endonucleases: NlaIV, BstYI, BamHI,
116
117
      AlwI, MboI,
                        DpnI, AflII, MseI, SspI, NsiI."
118
119
          (ix) FEATURE:
120
                 (A) NAME/KEY: misc_recomb
121
122
                 (B) LOCATION: 74..98
123
                 (C) IDENTIFICATION METHOD: experimental
                 (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
124
                        /standard name= "Multiple cloning site"
125
126
                        /label= MCS
127
                        /note= "A sequence specifying recognition sites
128
      for the
129
                        restriction endonucleases: ScaI, RsaI, HpaI,
130
      HincII, MseI, SfcI,
                        PstI, Fnu4HI, BbvI, PvuII, NspBII, AluI, EcoRI."
131
132
133
134
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
135
      CGGGATCCTT AAGAATATTA TGCATNNNNN AGTTTATTCT TGACANNNNN NNNNNNNNNT
136
137
      60 、
138
      GGTATAATAN NANAGTACTG TTAACTGCAG CTGAATTCGG
139
140
      100
141
      (2) INFORMATION FOR SEQ ID NO: 2:
142
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143

144 (i) SEQUENCE CHARACTERISTICS:

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145
                       (A) LENGTH: 113 base pairs
-->
                       (B) TYPE: nucleic acid
      146
      147
                       (C) STRANDEDNESS: double
      148
                       (D) TOPOLOGY: linear
      149
      150
                (ii) MOLECULE TYPE: DNA (genomic)
      151
      152
               (iii) HYPOTHETICAL: YES
      153
      154
                (iv) ANTI-SENSE: NO
      155
      156
      157
                (ix) FEATURE:
      158
                       (A) NAME/KEY: promoter
                       (B) LOCATION: 23..95
      159
                      (D) OTHER INFORMATION:/standard_name= "Artificial
      160
      161
                              promoter library"
      162
                              /note= "A degenerated sequence specifying a
      163
            mixture of
                             artificial temperature regulated promoters
      164
      165
            covering a wide range
      166
                              of expression in small steps in L. lactis"
      167
                (ix) FEATURE:
      168
      169
                       (A) NAME/KEY: misc feature
      170
                       (B) LOCATION: 23..49
                      (D) OTHER INFORMATION:/standard name= "Sequence
      171
      172
            providing
      173
                              temperature regulation to promoters"
      174
                              /note= "This sequence comprising two inverted
      175
           repeats separated
      176
                             by a short spacer provides temperature (heat
      177
            shock) regulation
      178
                             to promoters in Gram-positive bacteria"
      179
                (ix) FEATURE:
      180
      181
                      (A) NAME/KEY: misc feature
      182
                      (B) LOCATION:50..60
      183
                      (D) OTHER INFORMATION:/standard name= "Consensus
      184
                              sequence"
      185
                (ix) FEATURE:
      186
      187
                      (A) NAME/KEY: misc feature
      188
                      (B) LOCATION: 75..84
      189
                      (D) OTHER INFORMATION:/standard name= "Consensus
      190
                              sequence"
      191
                (ix) FEATURE:
      192
                      (A) NAME/KEY: misc feature
      193
      194
                      (B) LOCATION: 89..95
      195
                      (D) OTHER INFORMATION:/standard_name= "Consensus
      196
                             sequence"
      197
```

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```
(ix) FEATURE:
198
199
                (A) NAME/KEY: -35 signal
200
                (B) LOCATION:55..60
201
                (D) OTHER INFORMATION:/standard name= "-35 box"
202
203
          (ix) FEATURE:
                (A) NAME/KEY: -10_signal
204
                (B) LOCATION: 78..83
205
206
                (D) OTHER INFORMATION:/standard name= "Pribnow box"
207
208
          (ix) FEATURE:
209
                (A) NAME/KEY: misc recomb
210
                (B) LOCATION:3..22
211
                (D) OTHER INFORMATION:/standard name= "Multiple cloning
212
                       site"
                       /label= MCS
213
214
                       /note= "A sequence specifying recognition sites
     for the
215
                       restriction endonucleases: NlaIV, BstYI, BamHI,
216
217
     AlwI, MboI,
                       DpnI, HindIII, AluI, MseI (2 sites), SspI,
218
219
     AseI."
220
          (ix) FEATURE:
221
222
                (A) NAME/KEY: misc recomb
223
                (B) LOCATION:89..111
                (D) OTHER INFORMATION:/standard name= "Multiple cloning
224
225
                       site"
                       /label= MCS
226
227
                       /note= "A sequence specifying recognition sites
228
     for the
                       restriction endonucleases: ScaI, RsaI, SfcI,
229
230
     PstI, Fnu4HI, BbvI,
                       PvuII, NspBII, AluI, XbaI, MaeI, EcoRI, ApoI."
231
232
233
234
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
235
236
     CGGGATCCAA GCTTAATATT AATTAGCACT CNNNNNNNN GAGTGCTAAT TTTTTTGACA
237
238
     NNNNNNNN NNNTGGTAT AATANNANAG TACTGCAGCT GTCTAGAATT CGG
239
240
     113
241
242
      (2) INFORMATION FOR SEQ ID NO: 3:
243
244
           (i) SEQUENCE CHARACTERISTICS:
245
                (A) LENGTH: 199 base pairs
246
                (B) TYPE: nucleic acid
247
                (C) STRANDEDNESS: double
248
                (D) TOPOLOGY: linear
249
```

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```
250
          (ii) MOLECULE TYPE: DNA (genomic)
251
         (iii) HYPOTHETICAL: YES
252
253
254
          (iv) ANTI-SENSE: NO
255
256
          (vi) ORIGINAL SOURCE:
257
                 (A) ORGANISM: Saccharomyces cerevisiae
258
259
          (ix) FEATURE:
260
                 (A) NAME/KEY: protein bind
261
                 (B) LOCATION: 10..16
                 (D) OTHER INFORMATION:/function= "Activating promoters
262
263
      in
264
                        S. cerevisiae"
                        /bound_moiety= "GCN4 protein"
265
                        /standard name= "Upstream activating sequence"
266
                        /label= UAS GCN4p
267
                        /note= "A DNA sequence that specifies a binding
268
      site for the
269
                       GCN4 protein, which activates the transcription
270
271
     of genes
272
                        involved in aminoacid synthesis in S.
273
      cerevisiae."
                                  insutspace
274
          (ix) FEATURE:
275
276
                (A) NAME/KEY: TATA_signal
277
                (B) LOCATION: 67..72
278
                (D) OTHER INFORMATION:/standard_name= "TATA box"
279
          (ix) FEATURE:
280
281
                (A) NAME/KEY: misc_signal
282
                (B) LOCATION: 122..144
                (D) OTHER INFORMATION:/function= "Transcription
283
284
                        initiation"
                       /standard name= "TI box"
285
286
287
          (ix) FEATURE:
288
                (A) NAME/KEY: protein bind
289
                (B) LOCATION: 122..144
290
                (D) OTHER INFORMATION:/bound_moiety= "Arginine
291
      repressor"
                       /standard name= "arginine repressor binding
292
293
      site"
294
                       /label= argR
295
          (ix) FEATURE:
296
297
                (A) NAME/KEY: misc RNA
298
                (B) LOCATION: 145..192
299
                (D) OTHER INFORMATION:/function= "Spacer"
300
                       /standard name= "Part of native sequence for
301
     ARG8
302
                       gene incl. first codon"
```

303

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```
304
         (ix) FEATURE:
305
              (A) NAME/KEY: misc_recomb
306
              (B) LOCATION:3..8
              (D) OTHER INFORMATION:/standard name= "Recognition site
307
                     for restriction endonuclease EcoRI"
308
                     /label= EcoRI_site
309
310
311
         (ix) FEATURE:
312
              (A) NAME/KEY: misc recomb
313
              (B) LOCATION: 192...197
              (D) OTHER INFORMATION: /standard name= "Recognition site
314
315
                     for restriction endonuclease BamHI"
316
                     /label= BamHI site
317
         (ix) FEATURE:
318
              (A) NAME/KEY: promoter
319
              (B) LOCATION: 10..192
320
              (D) OTHER INFORMATION:/standard name= "Artificial
321
                    promoter library"
322
323
                     /note= "A degenerated sequence specifying a
     mixture of
324
                    artificial promoters covering a wide range of
325
326
     expression in
327
                   small steps in S. cerevisiae"
328
329
330
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
331
                                                                    some
332
     333
334
     335
336
337
     NCTCTTAAGT GCAAGTGACT GCGAACATTT TTTTCGTTTG TTAGAATAAT TCAAGAATCG
338
339
340
341
     CTACCAATCA TGGATCCCG
342
343
344
     (2) INFORMATION FOR SEQ ID NO: 4:
345
          (i) SEQUENCE CHARACTERISTICS:
346
347
              (A) LENGTH: 45 base pairs
              (B) TYPE: nucleic acid
348
              (C) STRANDEDNESS: double
349
350
              (D) TOPOLOGY: linear
351
352
        (ii) MOLECULE TYPE: DNA (genomic)
353
354
        (iii) HYPOTHETICAL: YES
```

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```
355
                (iv) ANTI-SENSE: NO
      356
      357
      358
                (vi) ORIGINAL SOURCE:
      359
                      (A) ORGANISM: Pseudomonas putida
      360
                (ix) FEATURE:
      361
                      (A) NAME/KEY: promoter
      362
      363
                      (B) LOCATION:1..45
      364
                      (C) IDENTIFICATION METHOD: experimental
      365
                      (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
      366
                             /standard name= "Artificial promoter library"
                             /note= "A degenerated sequence specifying a
      367
      368
           mixture of
      369
                             artificial promoterscovering a wide range of
      370
            expression in small
                             steps Pseudomonas putida"
      371
      372
      373
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
      374
                                                                           same
      375
      376
           NNNNNNNTT GRNNNNNNN NNNNNNNNN NTATRATNNN NNNNN
      377
            45
      378
      379
            (2) INFORMATION FOR SEQ ID NO: 5:
      380
      381
                 (i) SEQUENCE CHARACTERISTICS:
      382
                      (A) LENGTH: 60 base pairs
-->
                      (B) TYPE: nucleic acid
      383
      384
                      (C) STRANDEDNESS: double
      385
                      (D) TOPOLOGY: linear
      386
      387
                (ii) MOLECULE TYPE: DNA (genomic)
      388
               (iii) HYPOTHETICAL: YES
      389
      390
      391
                (iv) ANTI-SENSE: NO
      392
                (vi) ORIGINAL SOURCE:
      393
      394
                      (A) ORGANISM: Lactococcus lactis
      395
                (ix) FEATURE:
      396
      397
                      (A) NAME/KEY: promoter
      398
                      (B) LOCATION: 4..60
      399
                      (D) OTHER INFORMATION:/standard name= "Constitutional
      400
                             promoter"
      401
                             /label= Cp1
      402
      403
                                                                                   same
      404
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
      405
           CATACCGGAG TTTATTCTTG ACAGTTCCAC CTCGGGTTGA TATAATATCT CAGTACTGTT
      406
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407
      60
408
409
      (2) INFORMATION FOR SEQ ID NO: 6:
410
411
           (i) SEQUENCE CHARACTERISTICS:
412
                (A) LENGTH: 60 base pairs
413
                (B) TYPE: nucleic acid
414
415
                (C) STRANDEDNESS: double
416
                (D) TOPOLOGY: linear
417
         (ii) MOLECULE TYPE: DNA (genomic)
418
419
         (iii) HYPOTHETICAL: YES
420
421
         (iv) ANTI-SENSE: NO
422
423
          (vi) ORIGINAL SOURCE:
424
                (A) ORGANISM: Lactococcus lactis
425
426
427
          (ix) FEATURE:
                (A) NAME/KEY: promoter
428
                (B) LOCATION: 4...60
429
                (D) OTHER INFORMATION:/standard_name= "Constitutional
430
431
                       promoter"
                       /label= Cp10
432
433
434
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
435
                                                                            same
436
     CATGGCTTAG TTTATTCTTG ACAGGGTAGT ATCACTGTGA TATAATAGGA CAGTACTGTT
437
438
     60
439
440
      (2) INFORMATION FOR SEQ ID NO: 7:
442
           (i) SEQUENCE CHARACTERISTICS:
443
                (A) LENGTH: 59 base pairs
444
445
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
446
                (D) TOPOLOGY: linear
447
448
449
         (ii) MOLECULE TYPE: DNA (genomic)
450
         (iii) HYPOTHETICAL: YES
451
452
453
         (iv) ANTI-SENSE: NO
454
455
          (vi) ORIGINAL SOURCE:
456
                (A) ORGANISM: Lactococcus lactis
457
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```
458
                (ix) FEATURE:
      459
                      (A) NAME/KEY: promoter
      460
                      (B) LOCATION:4..59
      461
                      (D) OTHER INFORMATION:/standard_name= "Constitutional
      462
                             promoter"
                             /label= Cp11
      463
      464
      465
                                                                                   some
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
      466
      467
      468
            CATAAGTGAG TTTATTCTTG ACCCGGACGC CCCCCTTTGA TATAATAAGT AGTACTGTT
      469
      470
      471
            (2) INFORMATION FOR SEQ ID NO: 8:
      472
                 (i) SEQUENCE CHARACTERISTICS:
      473
      474
                      (A) LENGTH: 60 base pairs
                      (B) TYPE: nucleic acid
      475
                      (C) STRANDEDNESS: double
      476
      477
                      (D) TOPOLOGY: linear
      478
      479
                (ii) MOLECULE TYPE: DNA (genomic)
      480
               (iii) HYPOTHETICAL: YES
      481
      482
      483
                (iv) ANTI-SENSE: NO
      484
      485
                (vi) ORIGINAL SOURCE:
      486
                      (A) ORGANISM: Lactococcus lactis
      487
                (ix) FEATURE:
      488
      489
                      (A) NAME/KEY: promoter
      490
                      (B) LOCATION: 4..60
                      (D) OTHER INFORMATION:/standard name= "Constitutional
      491
      492
                             promoter"
      493
                             /label= Cp12
      494
      495
                                                                                   same
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
      496
      497
            CATATACAAG TTTATTCTTG ACACTAGTCG GCCAAAATGA TATAATACCT GAGTACTGTT
      498
      499
            60
      500
      501
      502
            (2) INFORMATION FOR SEQ ID NO: 9:
      503
      504
                 (i) SEQUENCE CHARACTERISTICS:
      505
                      (A) LENGTH: 60 base pairs
-->
      506
                      (B) TYPE: nucleic acid
      507
                      (C) STRANDEDNESS: double
      508
                      (D) TOPOLOGY: linear
```

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```
509
                (ii) MOLECULE TYPE: DNA (genomic)
      510
      511
      512
               (iii) HYPOTHETICAL: YES
      513
      514
                (iv) ANTI-SENSE: NO
      515
                (vi) ORIGINAL SOURCE:
      516
      517
                      (A) ORGANISM: Lactococcus lactis
      518
      519
                (ix) FEATURE:
      520
                      (A) NAME/KEY: promoter
                      (B) LOCATION: 4..60
      521
      522
                      (D) OTHER INFORMATION:/standard name= "Constitutional
                             promoter"
      523
      524
                             /label= Cp13
      525
      526
      527
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
      528
            CATGCTTTAC TTTATTCTTG ACAAAACCAC CAGCTTTTGG TATAATACGT GAGAACTGTT
      529
      530
            60
      531
      532
            (2) INFORMATION FOR SEQ ID NO: 10:
      533
      534
      535
                 (i) SEQUENCE CHARACTERISTICS:
      536
                      (A) LENGTH: 60 base pairs
-->
      537
                      (B) TYPE: nucleic acid
                      (C) STRANDEDNESS: double
      538
                      (D) TOPOLOGY: linear
      539
      540
      541
                (ii) MOLECULE TYPE: DNA (genomic)
      542
               (iii) HYPOTHETICAL: YES
      543
      544
      545
                (iv) ANTI-SENSE: NO
      546
                (vi) ORIGINAL SOURCE:
      547
                      (A) ORGANISM: Lactococcus lactis
      548
      549
                (ix) FEATURE:
      550
                      (A) NAME/KEY: promoter
      551
      552
                      (B) LOCATION:4..60
      553
                      (D) OTHER INFORMATION:/standard name= "Constitutional
      554
                             promoter"
                             /label= Cp14
      555
      556
      557
      558
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
      559
      560
           CATGACGGAG TTTATTCTTG ACACAGGTAT GGACTTATGA TATAATAAAA CAGTACTGTT
```

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```
561
      60
562
563
      (2) INFORMATION FOR SEQ ID NO: 11:
564
565
566
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 60 base pairs
567
                (B) TYPE: nucleic acid
568
569
                (C) STRANDEDNESS: double
570
                (D) TOPOLOGY: linear
571
          (ii) MOLECULE TYPE: DNA (genomic)
572
573
         (iii) HYPOTHETICAL: YES
574
575
          (iv) ANTI-SENSE: NO
576
577
          (vi) ORIGINAL SOURCE:
578
                (A) ORGANISM: Lactococcus lactis
579
580
581
          (ix) FEATURE:
582
                (A) NAME/KEY: promoter
                (B) LOCATION: 4...60
583
                (D) OTHER INFORMATION:/standard_name= "Constitutional
584
                       promoter"
585
586
                       /label= Cp15
587
588
589
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
590
     CATTACNTAG TTNATTCTTG ACAGAATTAC GATTCGCTGG TATAATATAT CAGTACTGTT
591
592
     60
593
594
595
      (2) INFORMATION FOR SEQ ID NO: 12:
596
597
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 58 base pairs
598
                (B) TYPE: nucleic acid
599
                (C) STRANDEDNESS: double
600
                (D) TOPOLOGY: linear
601
602
          (ii) MOLECULE TYPE: DNA (genomic)
603
604
605
         (iii) HYPOTHETICAL: YES
606
607
          (iv) ANTI-SENSE: NO
608
609
          (vi) ORIGINAL SOURCE:
610
                (A) ORGANISM: Lactococcus lactis
611
```

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```
(ix) FEATURE:
612
                (A) NAME/KEY: promoter
613
614
                (B) LOCATION:4..58
                (D) OTHER INFORMATION:/standard_name= "Constitutional
615
616
                       promoter"
617
                       /label= Cp16
618
619
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
620
621
      CATTGTGTAG TTTATTCTTG ACAGCTATGA GTCAATTTGG TATAATAACA GTACTCAG
622
623
624
625
      (2) INFORMATION FOR SEQ ID NO: 13:
626
           (i) SEQUENCE CHARACTERISTICS:
627
                (A) LENGTH: 59 base pairs
628
                (B) TYPE: nucleic acid
629
630
                (C) STRANDEDNESS: double
631
                (D) TOPOLOGY: linear
632
633
          (ii) MOLECULE TYPE: DNA (genomic)
634
         (iii) HYPOTHETICAL: YES
635
636
          (iv) ANTI-SENSE: NO
637
638
          (vi) ORIGINAL SOURCE:
639
                (A) ORGANISM: Lactococcus lactis
640
641
          (ix) FEATURE:
642
643
                (A) NAME/KEY: promoter
                (B) LOCATION: 4..59
644
                (D) OTHER INFORMATION:/standard name= "Constitutional
645
646
                       promoter"
                       /label= Cp17
647
648
649
650
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
651
     CATTCTGGAG TTTATTCTTG ACCGCTCAGT ATGCAGTGGT ATAATAGTAC AGTACTGTT
652
653
654
655
      (2) INFORMATION FOR SEQ ID NO: 14:
656
           (i) SEQUENCE CHARACTERISTICS:
657
658
                (A) LENGTH: 58 base pairs
659
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
660
                (D) TOPOLOGY: linear
661
662
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```
(ii) MOLECULE TYPE: DNA (genomic)
663
664
         (iii) HYPOTHETICAL: YES
665
666
667
          (iv) ANTI-SENSE: NO
668
          (vi) ORIGINAL SOURCE:
669 -
                (A) ORGANISM: Lactococcus lactis
670
671
672
          (ix) FEATURE:
                (A) NAME/KEY: promoter
673
674
                (B) LOCATION:4..58
                (D) OTHER INFORMATION:/standard name= "Constitutional
675
676
                       promoter"
677
                       /label= Cp18
678
679
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
680
681
      CATTTTGCAG TTTATTCTTG ACATTGTGTG CTTCGGGTGT ATAATACTAA GTACTGTT
682
683
684
      (2) INFORMATION FOR SEQ ID NO: 15:
685
686
687
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 58 base pairs
688
                (B) TYPE: nucleic acid
689
                (C) STRANDEDNESS: double
690
                (D) TOPOLOGY: linear
691
692
          (ii) MOLECULE TYPE: DNA (genomic)
693
694
695
         (iii) HYPOTHETICAL: YES
696
          (iv) ANTI-SENSE: NO
697
698
699
          (vi) ORIGINAL SOURCE:
700
                (A) ORGANISM: Lactococcus lactis
701
          (ix) FEATURE:
702
703
                (A) NAME/KEY: promoter
704
                (B) LOCATION:4..58
705
                (D) OTHER INFORMATION:/standard name= "Constitutional
706
                       promoter"
707
                       /label= Cp19
708
709
710
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
711
712
     CATCGCTTAG TTTTTCTTGA CAGGAGGGAT CCGGGTTGAT ATAATAGTTA GTACTGTT
713
     58
714
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715
            (2) INFORMATION FOR SEQ ID NO: 16:
      716
      717
                 (i) SEQUENCE CHARACTERISTICS:
-->
      718
                      (A) LENGTH: 60 base pairs
                      (B) TYPE: nucleic acid
      719
      720
                      (C) STRANDEDNESS: double
                      (D) TOPOLOGY: linear
      721
      722
      723
                (ii) MOLECULE TYPE: DNA (genomic)
      724
      725
               (iii) HYPOTHETICAL: YES
      726
      727
                (iv) ANTI-SENSE: NO
      728
             (vi) ORIGINAL SOURCE:
      729
                      (A) ORGANISM: Lactococcus lactis
      730
      731
                (ix) FEATURE:
      732
                      (A) NAME/KEY: promoter
      733
                      (B) LOCATION: 4..60
      734
      735
                      (D) OTHER INFORMATION: /standard name= "Constitutional
      736
                             promoter"
                             /label= Cp2
      737
      738
      739
      740
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
      741
      742
           CATTTGCTAG TTTATTCTTG ACATGAAGCG TGCCTAATGG TATATTACTT GAGTACTGTT
      743
            60
      744
      745
      746
            (2) INFORMATION FOR SEQ ID NO: 17:
      747
                 (i) SEQUENCE CHARACTERISTICS:
      748
      749
                      (A) LENGTH: 60 base pairs
      750
                      (B) TYPE: nucleic acid
                      (C) STRANDEDNESS: double
      751
      752
                      (D) TOPOLOGY: linear
      753
                (ii) MOLECULE TYPE: DNA (genomic)
      754
      755
               (iii) HYPOTHETICAL: YES
      756
      757
      758
                (iv) ANTI-SENSE: NO
      759
      760
                (vi) ORIGINAL SOURCE:
      761
                      (A) ORGANISM: Lactococcus lactis
      762
                (ix) FEATURE:
      763
      764
                      (A) NAME/KEY: promoter
      765
                      (B) LOCATION: 4..60
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816

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INPUT SET: S34681.raw (D) OTHER INFORMATION:/standard_name= "Constitutional 766 767 promoter" 768 /label= Cp20 769 770 771 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17: 772 CATGGGTGAG TTTATTCTTG ACAGTGCGGC CNGGGGCTGA TATCATAGCA GAGTACTATT 773 774 60 775 776 777 (2) INFORMATION FOR SEQ ID NO: 18: 778 779 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs 780 781 (B) TYPE: nucleic acid 782 (C) STRANDEDNESS: double (D) TOPOLOGY: linear 783 784 (ii) MOLECULE TYPE: DNA (genomic) 785 786 (iii) HYPOTHETICAL: YES 787 788 789 (iv) ANTI-SENSE: NO 790 791 (vi) ORIGINAL SOURCE: 792 (A) ORGANISM: Lactococcus lactis 793 (ix) FEATURE: 794 (A) NAME/KEY: promoter 795 796 (B) LOCATION:4..59 797 (D) OTHER INFORMATION:/standard name= "Constitutional 798 promoter" 799 /label= Cp21 800 801 802 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18: CATTACCGAG TTTATTCTTG ACACCGTTTA TCGGGGTTGT ATAATACTAT AGTACTGTT 804 805 59 806 807 (2) INFORMATION FOR SEQ ID NO: 19: 808 809 (i) SEQUENCE CHARACTERISTICS: 810 (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid 811. (C) STRANDEDNESS: double 812 813 (D) TOPOLOGY: linear 814 815 (ii) MOLECULE TYPE: DNA (genomic)

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```
(iii) HYPOTHETICAL: YES
817
818
819
          (iv) ANTI-SENSE: NO
820
821
          (vi) ORIGINAL SOURCE:
822
                (A) ORGANISM: Lactococcus lactis
823
          (ix) FEATURE:
824
825
                (A) NAME/KEY: promoter
                (B) LOCATION: 4..60
826
827
                (D) OTHER INFORMATION:/standard name= "Constitutional
828
                       promoter"
829
                       /label= Cp23
830
831
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
832
833
     CATGTAGGAG TTTATTCTTG ACAGATTAGT TAGGGGGTGG TATAATATCT CAGTACTGTT
834
835
      60
836
837
838
      (2) INFORMATION FOR SEQ ID NO: 20:
839
840
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 60 base pairs
841
                (B) TYPE: nucleic acid
842
843
                (C). STRANDEDNESS: double
844
                (D) TOPOLOGY: linear
845
846
          (ii) MOLECULE TYPE: DNA (genomic)
847
848
         (iii) HYPOTHETICAL: YES
849
850
          (iv) ANTI-SENSE: NO
851
852
          (vi) ORIGINAL SOURCE:
853
                (A) ORGANISM: Lactococcus lactis
854
          (ix) FEATURE:
855
856
                (A) NAME/KEY: promoter
                (B) LOCATION: 4..60
857
                (D) OTHER INFORMATION:/standard_name= "Constitutional
858
859
                       promoter"
860
                       /label= Cp24
861
862
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
863
864
     CATGGGTAAG TTTATTCTTC ACACTATCTG GGCCCGATGG TATAATAAGT GACTACTGTT
865
866
867
868
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	_	
	869	(2) INFORMATION FOR SEQ ID NO: 21:
	870	
	871	(i) SEQUENCE CHARACTERISTICS:
>	872	(A) LENGTH: 59 base pairs
	873	(B) TYPE: nucleic acid
	874	(C) STRANDEDNESS: double
	875	(D) TOPOLOGY: linear
	876	
	877	(ii) MOLECULE TYPE: DNA (genomic)
	878	
	879	(iii) HYPOTHETICAL: YES
	880	
	881	(iv) ANTI-SENSE: NO
	882	
	883	(vi) ORIGINAL SOURCE:
	884	(A) ORGANISM: Lactococcus lactis
	885	()
	886	(ix) FEATURE:
	887	(A) NAME/KEY: promoter
٠	888	(B) LOCATION:359
	889	(D) OTHER INFORMATION:/standard_name= "Constitutional
	890	promoter"
	891	/label= Cp25
	892	
	893	(')
	894	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
	895	CHEMICAGO CHI THOUTHAN AND CHARLES AND CHA
	896	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21: CTTTGGCAGT TTATTCTTGA CATGTAGTGA GGGGGCTGGT ATAATCACAT AGTACTGTT 59
	897 898	59
	030	
	899	(2) INFORMATION FOR SEQ ID NO: 22:
	900	·
	901	(i) SEQUENCE CHARACTERISTICS:
>	902	(A) LENGTH: 60 base pairs
	903	(B) TYPE: nucleic acid
	904	(C) STRANDEDNESS: double
	905	(D) TOPOLOGY: linear
	906	
	907	(ii) MOLECULE TYPE: DNA (genomic)
	908	
	909	(iii) HYPOTHETICAL: YES
	910	r
	911	(iv) ANTI-SENSE: NO
	912	
	913	(vi) ORIGINAL SOURCE:
	914	(A) ORGANISM: Lactococcus lactis
	915	
	916	(ix) FEATURE:
	917	(A) NAME/KEY: promoter
	918	(B) LOCATION: 460
	919	(D) OTHER INFORMATION:/standard name= "Constitutional

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		INPUT SET: S34	34681.raw	
	920	promoter"		
	921	/label= Cp26		
	922	-		
	923			
	924	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:		
	925		ν	
	926	CATTCTACAG TTTATTCTTG ACATTGCACT GTCCCCCTGG TATAATAACT ATACATGCAT	$\mathcal{M}^{\mathcal{M}}$	
	927	60	///	
	928		/ *	
	929			
	930	(2) INFORMATION FOR SEQ ID NO: 23:		
	931			
	932	(i) SEQUENCE CHARACTERISTICS:		
>	933	(A) LENGTH: 60 base pairs		
	934	(B) TYPE: nucleic acid		
	935	(C) STRANDEDNESS: double		
	936	(D) TOPOLOGY: linear		
	937			
	938	(ii) MOLECULE TYPE: DNA (genomic)		
	939			
	940	(iii) HYPOTHETICAL: YES		
	941			
	942	(iv) ANTI-SENSE: NO	•	
	943			
	944	(vi) ORIGINAL SOURCE:		
•	945	(A) ORGANISM: Lactococcus lactis		
	946			
	947	(ix) FEATURE:		
	948	(A) NAME/KEY: promoter		
	949	(B) LOCATION: 460		
	950	(D) OTHER INFORMATION:/standard_name= "Constitutional		
	951	promoter"		
	952	/label= Cp28		
	953			
	954			
	955	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:	,	
	956		<i>\\</i>	
	957 958	CATGGGGCCG TTTATTCTTG ACAACGGCGA GCAGACCTGG TATAATAATA TAGTACTGTT	$\mathcal{N}^{\mathcal{N}}$	
		60	pame	
	959 960	•	,	
-	961	(2) INFORMATION FOR SEQ ID NO: 24:		
	962	(2) INFORMATION FOR BEG ID NO: 54:		
	963	(i) SEQUENCE CHARACTERISTICS:		
>	964	(A) LENGTH: 59 base pairs		
	965	(B) TYPE: nucleic acid		
	966	(C) STRANDEDNESS: double		
	967	(D) TOPOLOGY: linear		
	968	(D) IOFOLOGI. IIMEGI		
	969	(ii) MOLECULE TYPE: DNA (genomic)		
	970	(II) NODECODE IIIB. DAA (GCNOMIC)		
	270			

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INPUT SET: S34681.raw (iii) HYPOTHETICAL: YES 971 972 973 (iv) ANTI-SENSE: NO 974 975 (vi) ORIGINAL SOURCE: 976 (A) ORGANISM: Lactococcus lactis 977 (ix) FEATURE: 978 979 (A) NAME/KEY: promoter 980 (B) LOCATION:4..59 981 (D) OTHER INFORMATION:/standard name= "Constitutional 982 promoter" 983 /label= Cp29 984 same 985 986 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24: 987 CATCGGTAAG TTATTCTTGA CATCTCAGGG GGGACGTGGT ATAATAACTG AGTACTGTT 988 989 59 990 991 (2) INFORMATION FOR SEQ ID NO: 25: 992 993 (i) SEQUENCE CHARACTERISTICS: 994 (A) LENGTH: 60 base pairs 995 (B) TYPE: nucleic acid 996 (C) STRANDEDNESS: double 997 (D) TOPOLOGY: linear 998 999 (ii) MOLECULE TYPE: DNA (genomic) 1000 1001 (iii) HYPOTHETICAL: YES 1002 1003 (iv) ANTI-SENSE: NO 1004 (vi) ORIGINAL SOURCE: 1005 1006 (A) ORGANISM: Lactococcus lactis 1007 1008 (ix) FEATURE: (A) NAME/KEY: promoter 1009 1010 (B) LOCATION: 4..60 1011 (D) OTHER INFORMATION:/standard name= "Constitutional 1012 promoter" Same 1013 /label= Cp3 1014 1015 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25: 1016 1017 CATCCTGTAG TTTATTCTTG ACACACGTNN TTAGCTGTGG TATAATAGGA GAGTACTGTT 1018 1019 60 1020 1021

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1023
            (i) SEQUENCE CHARACTERISTICS:
1024
1025
                 (A) LENGTH: 60 base pairs
1026
                 (B) TYPE: nucleic acid
1027
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear
1028
1029
1030
           (ii) MOLECULE TYPE: DNA (genomic)
1031
          (iii) HYPOTHETICAL: YES
1032
1033
1034
           (iv) ANTI-SENSE: NO
1035
1036
           (vi) ORIGINAL SOURCE:
1037
                 (A) ORGANISM: Lactococcus lactis
1038
           (ix) FEATURE:
1039
                 (A) NAME/KEY: promoter
1040
                 (B) LOCATION:4..60
1041
                 (D) OTHER INFORMATION:/standard name= "Constitutional
1042
1043
                        promoter"
1044
                         /label= Cp30
1045
1046
1047
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
1048
       CATGACAGAG TTTATTCTTG ACAGTATTGG GTTACTTTGG TATAATAGTT GAGTACTGTT
1049
1050
1051
1052
1053
       (2) INFORMATION FOR SEQ ID NO: 27:
1054
1055
            (i) SEQUENCE CHARACTERISTICS:
1056
                 (A) LENGTH: 60 base pairs
                 (B) TYPE: nucleic acid
1057
1058
                 (C) STRANDEDNESS: double
1059
                 (D) TOPOLOGY: linear
1060
           (ii) MOLECULE TYPE: DNA (genomic)
1061
1062
          (iii) HYPOTHETICAL: YES
1063
1064
1065
           (iv) ANTI-SENSE: NO
1066
1067
           (vi) ORIGINAL SOURCE:
1068
                 (A) ORGANISM: Lactococcus lactis
1069
           (ix) FEATURE:
1070
1071
                 (A) NAME/KEY: promoter
1072
                 (B) LOCATION: 4..60
1073
                 (D) OTHER INFORMATION:/standard name= "Constitutional
1074
                        promoter"
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	INPUT SET:		
	1075	/label= Cp32	
•	1076	, 14361- 6551	
	1077		
	1077	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:	
		(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 27:	
	1079	CARL COCCA C TERM THOUSE A CARL THOUSE COCCATON TO THE TAX COCCATON TO THE COC	V
	1080	CATACGGGAG TTTATTCTTG ACATATTGCC GGTGTGTTGG TATAATAACT TAGTACTGTT	$\sim N^{N}$
	1081	60	
	1082		ŀ
	1083		
	1004	(2) INFORMATION FOR GEO ID NO. 20.	· · · · · · · · · · · · · · · · · · ·
	1084 1085	(2) INFORMATION FOR SEQ ID NO: 28:	
		(+) CHOUSINGS GUADA CHIEF CHIEF	
	1086	(i) SEQUENCE CHARACTERISTICS:	
>	1087	(A) LENGTH: 60 base pairs	
	1088	(B) TYPE: nucleic acid	
	1089	(C) STRANDEDNESS: double	
	1090	(D) TOPOLOGY: linear	
	1091		
	1092	(ii) MOLECULE TYPE: DNA (genomic)	
	1093		
	1094	(iii) HYPOTHETICAL: YES	
	1095		
	1096	(iv) ANTI-SENSE: NO	
	1097		
	1098	(vi) ORIGINAL SOURCE:	
	1099	(A) ORGANISM: Lactococcus lactis	
	1100		
	1101	(ix) FEATURE:	
	1102	(A) NAME/KEY: promoter	
	1103	(B) LOCATION: 460	
	1104	(D) OTHER INFORMATION:/standard name= "Constitutional	
	1105	promoter"	
	1106	/label= Cp33	
	1107	/label- Cp33	
	1107		
		(wi) GEOMENGE DECORTONION, GEO. ID NO. 20.	
	1109	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:	•/
	1110		200
	1111	CATGTTGGAG TTTATTCTTG ACATACAATT ACTGCAGTGA TATAATAGGT GAGTACTGTT	20
	1112	60	/Y
	1113		•
	1114		
-	1115	(2) INFORMATION FOR SEQ ID NO: 29:	
	1116	/-,	
	1117	(i) SEQUENCE CHARACTERISTICS:	
>	1118	(A) LENGTH: 60 base pairs	
,	1119	(B) TYPE: nucleic acid	
	1120	(C) STRANDEDNESS: double	
	1121	(D) TOPOLOGY: linear	
	1122	// //	
	1123	(ii) MOLECULE TYPE: DNA (genomic)	
	1124		
	1125	(iii) HYPOTHETICAL: YES	

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```
1126
           (iv) ANTI-SENSE: NO
1127
1128
1129
           (vi) ORIGINAL SOURCE:
1130
                 (A) ORGANISM: Lactococcus lactis
1131
           (ix) FEATURE:
1132
                 (A) NAME/KEY: promoter
1133
1134
                 (B) LOCATION:4..60
1135
                 (D) OTHER INFORMATION:/standard name= "Constitutional
1136
                        promoter"
1137
                        /label= Cp34
1138
1139
1140
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:
1141
       CATCGCGAAG TTTATTCTTC ACACACCGCA GAACTTGTGG TATAATACAA CAGTACTGTT
1142
1143
1144
1145
1146
       (2) INFORMATION FOR SEQ ID NO: 30:
1147
1148
            (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 59 base pairs
1149
                 (B) TYPE: nucleic acid
1150
1151
                 (C) STRANDEDNESS: double
1152
                 (D) TOPOLOGY: linear
1153
1154
          (ii) MOLECULE TYPE: DNA (genomic)
1155
          (iii) HYPOTHETICAL: YES
1156
1157
          (iv) ANTI-SENSE: NO
1158
1159
1160
          (vi) ORIGINAL SOURCE:
1161
                 (A) ORGANISM: Lactococcus lactis
1162
           (ix) FEATURE:
1163
1164
                 (A) NAME/KEY: promoter
                 (B) LOCATION:4..59
1165
                 (D) OTHER INFORMATION:/standard_name= "Constitutional
1166
1167
                        promoter"
                        /label= Cp37
1168
1169
1170
1171
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:
1172
1173
      CATCATTAAG TTTATTCTTC ACATTGGCCG GAATTGTTGT ATAATACCTT AGTACTGTT
1174
      59
1175
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1177
 1178
             (i) SEQUENCE CHARACTERISTICS:
 1179
                   (A) LENGTH: 60 base pairs
 1180
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
 1181
 1182
                   (D) TOPOLOGY: linear
 1183
 1184
            (ii) MOLECULE TYPE: DNA (genomic)
 1185
           (iii) HYPOTHETICAL: YES
 1186
 1187
            (iv) ANTI-SENSE: NO
 1188
 1189
 1190
            (vi) ORIGINAL SOURCE:
 1191
                  (A) ORGANISM: Lactococcus lactis
 1192
 1193
            (ix) FEATURE:
                  (A) NAME/KEY: promoter
 1194
                  (B) LOCATION: 4..60
 1195
                  (D) OTHER INFORMATION:/standard name= "Constitutional
 1196
 1197
                         promoter"
 1198
                          /label= Cp38
 1199
 1200
 1201
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:
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        CATAGAGAAG TTTATTCTTG ACAGCTAACT TGGCCTTTGA TATAATACAT GAGTACTGTT
 1203
 1204
 1205
 1206
 1207
        (2) INFORMATION FOR SEQ ID NO: 32:
 1208
 1209
             (i) SEQUENCE CHARACTERISTICS:
 1210
                  (A) LENGTH: 60 base pairs
                  (B) TYPE: nucleic acid
 1211
 1212
                  (C) STRANDEDNESS: double
 1213
                  (D) TOPOLOGY: linear
 1214
           (ii) MOLECULE TYPE: DNA (genomic)
 1215
 1216
           (iii) HYPOTHETICAL: YES
 1217
 1218
 1219
            (iv) ANTI-SENSE: NO
 1220
 1221
            (vi) ORIGINAL SOURCE:
 1222
                  (A) ORGANISM: Lactococcus lactis
 1223
            (ix) FEATURE:
. 1224
 1225
                  (A) NAME/KEY: promoter
 1226
                  (B) LOCATION:4..60
 1227
                  (D) OTHER INFORMATION:/standard_name= "Constitutional
 1228
                         promoter"
```

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	INPUT SET: S34681.ray			
	1229			
	1230			
	1231	·		
	1232	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:		
	1232	(MI) begoined beschillion. Beg is no. 32.		
	1234	CATTGCGAAG TTTATTCTTG ACAGTACGTT TTTACCATGA TATAATAGTA TAGTACTGTT	كور	
	1235	60	^ / /	
	1236		/20	
	1237		,	
	1257			
	1238	(2) INFORMATION FOR SEQ ID NO: 33:		
	1239			
	1240	(i) SEQUENCE CHARACTERISTICS:		
>	1241	(A) LENGTH: 60 base pairs		
	1242	(B) TYPE: nucleic acid		
	1243	(C) STRANDEDNESS: double		
	1244	(D) TOPOLOGY: linear	•	
•	1245			
	1246	(ii) MOLECULE TYPE: DNA (genomic)		
	1247			
	1248	(iii) HYPOTHETICAL: YES		
	1249			
	1250	(iv) ANTI-SENSE: NO		
	1251			
	1252	(vi) ORIGINAL SOURCE:		
	1253	(A) ORGANISM: Lactococcus lactis		
	1254			
	1255	(ix) FEATURE:		
	1256	(A) NAME/KEY: promoter		
	1257	(B) LOCATION: 460		
	1258	(D) OTHER INFORMATION:/standard_name= "Constitutional		
	1259	promoter"		
	1260	/label= Cp4 ,		
	1261			
	1262	•		
	1263	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:		
	1264		ν	
	1265	GATGTTTTAG TTTATTCTTG ACACCGTATC GTGCGCGTGA TATAATCGGG ATCCTTAAGA	$\mathcal{N}^{\mathcal{N}}$	
	1266	60	$\mathcal{N}^{\mathcal{U}}$	
	1267		/	
	1268			
	1269	(2) INFORMATION FOR SEQ ID NO: 34:		
	1270	/-/		
	1271	(i) SEOUENCE CHARACTERISTICS:		
>	1272	(A) LENGTH: 59 base pairs		
-	1273	(B) TYPE: nucleic acid		
	1274	(C) STRANDEDNESS: double		
	1275	(D) TOPOLOGY: linear		
	1276	(2) 1010201 244004		
	1277	(ii) MOLECULE TYPE: DNA (genomic)		
	1278	(,		
	1279	(iii) HYPOTHETICAL: YES		
	, _	,,		

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```
1280
           (iv) ANTI-SENSE: NO
1281
1282
           (vi) ORIGINAL SOURCE:
1283
1284
                 (A) ORGANISM: Lactococcus lactis
1285
           (ix) FEATURE:
1286
1287
                 (A) NAME/KEY: promoter
1288
                 (B) LOCATION: 4
1289
                 (D) OTHER INFORMATION:/standard name= "Constitutional
1290
                        promoter"
                        /label= Cp40
1291
1292
1293
1294
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
1295
       CATAGAACAG TTTATTCTTG ACATTGAATA AGAAGGCTGA TATAATAGCC AGTACTGTT
1296
1297
1298
       (2) INFORMATION FOR SEQ ID NO: 35:
1299
1300
1301
            (i) SEQUENCE CHARACTERISTICS:
1302
                 (A) LENGTH: 60 base pairs
                 (B) TYPE: nucleic acid
1303
                 (C) STRANDEDNESS: double
1304
1305
                 (D) TOPOLOGY: linear
1306
1307
           (ii) MOLECULE TYPE: DNA (genomic)
1308
          (iii) HYPOTHETICAL: YES
1309
1310
           (iv) ANTI-SENSE: NO
1311
1312
1313
           (vi) ORIGINAL SOURCE:
1314
                 (A) ORGANISM: Lactococcus lactis
1315
1316
           (ix) FEATURE:
1317
                 (A) NAME/KEY: promoter
1318
                 (B) LOCATION:4..60
1319
                 (D) OTHER INFORMATION:/standard name= "Constitutional
1320
                        promoter"
1321
                        /label= Cp41
1322
1323
1324
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
1325
      CATCCGCAAG TTTATTCTTG ACAGCTGAAT GTAGACGTGG TATAATAGTT AAGTACTGTT
1326
1327
       60
1328
1329
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```
1331
            (i) SEQUENCE CHARACTERISTICS:
1332
                 (A) LENGTH: 60 base pairs
1333
1334
                 (B) TYPE: nucleic acid
1335
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear
1336
1337
           (ii) MOLECULE TYPE: DNA (genomic)
1338
1339
1340
          (iii) HYPOTHETICAL: YES
1341
1342
          (iv) ANTI-SENSE: NO
1343
1344
          (vi) ORIGINAL SOURCE:
1345
                 (A) ORGANISM: Lactococcus lactis
1346
           (ix) FEATURE:
1347
                 (A) NAME/KEY: promoter
1348
                 (B) LOCATION:4..60
1349
                 (D) OTHER INFORMATION:/standard_name= "Constitutional
1350
1351
                        promoter"
1352
                        /label= Cp42
1353
1354
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:
1355
1356
      CATTCGTAAG TTTATTCTTG ACACCTGAGA TGAGGCGTGA TATAATAAAT AAGTACTGTT
1357
1358
1359
1360
       (2) INFORMATION FOR SEQ ID NO: 37:
1361
1362
            (i) SEQUENCE CHARACTERISTICS:
1363
1364
                 (A) LENGTH: 59 base pairs
                 (B) TYPE: nucleic acid
1366
                 (C) STRANDEDNESS: double
1367
                 (D) TOPOLOGY: linear
1368
       (ii) MOLECULE TYPE: DNA (genomic)
1369
1370
1371
         (iii) HYPOTHETICAL: YES
1372
          (iv) ANTI-SENSE: NO
1373
1374
1375
           (vi) ORIGINAL SOURCE:
1376
                 (A) ORGANISM: Lactococcus lactis
1377
1378
           (ix) FEATURE:
1379
                 (A) NAME/KEY: promoter
1380
                 (B) LOCATION: 4...59
1381
                 (D) OTHER INFORMATION:/standard name= "Constitutional
1382
                        promoter"
```

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```
/label= Cp44
1383
1384
1385
1386
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
1387
1388
       CATCGGGTAG TTTATTCTTG ACAATTAAGT AGAGCCTGAT ATAATAGTTC AGTACTGTT
1389
1390
       (2) INFORMATION FOR SEQ ID NO: 38:
1391
1392
1393
            (i) SEQUENCE CHARACTERISTICS:
1394
                 (A) LENGTH: 59 base pairs
                 (B) TYPE: nucleic acid
1395
1396
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear
1397
1398
           (ii) MOLECULE TYPE: DNA (genomic)
1399
1400
          (iii) HYPOTHETICAL: YES
1401
1402
           (iv) ANTI-SENSE: NO
1403
1404
           (vi) ORIGINAL SOURCE:
1405
1406
                 (A) ORGANISM: Lactococcus lactis
1407
1408
           (ix) FEATURE:
                 (A) NAME/KEY: promoter
1409
                 (B) LOCATION:4..59
1410
1411
                 (C) IDENTIFICATION METHOD: experimental
1412
                 (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1413
                        /standard name= "Constitutional promoter"
                        /label= Cp5
1414
1415
1416
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
1417
1418
      CATGGGGGAG TTTATTCTTG ACATCATCTT CGTAGCCTGG TATACTACAT GAGTATGTT
1419
1420
       59
1421
       (2) INFORMATION FOR SEQ ID NO: 39:
1422
1423
1424
            (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 60 base pairs
1425
                 (B) TYPE: nucleic acid
1426
                 (C) STRANDEDNESS: double
1427
                 (D) TOPOLOGY: linear
1428
1429
           (ii) MOLECULE TYPE: DNA (genomic)
1430
1431
1432
          (iii) HYPOTHETICAL: YES
1433
```

1484

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```
(iv) ANTI-SENSE: NO
1434
                                                                         . .
1435
1436
           (vi) ORIGINAL SOURCE:
1437
                  (A) ORGANISM: Lactococcus lactis
1438
           (ix) FEATURE:
1439
1440
                  (A) NAME/KEY: promoter
                  (B) LOCATION:4..60
1441
                  (D) OTHER INFORMATION:/standard name= "Constitutional
1442
                        promoter"
1443
1444
                        /label= Cp6
1445
1446
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
1447
1448
       CATGTGGGAG TTTATTCTTG ACACAGATAT TTCCGGATGA TATAATAACT GAGTACTGTT
1449
1450
1451
1452
       (2) INFORMATION FOR SEQ ID NO: 40:
1453
1454
1455
            (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 60 base pairs
1456
                  (B) TYPE: nucleic acid
1457
                  (C) STRANDEDNESS: double
1458
1459
                  (D) TOPOLOGY: linear
1460
1461
           (ii) MOLECULE TYPE: DNA (genomic)
1462
1463
          (iii) HYPOTHETICAL: YES
1464
           (iv) ANTI-SENSE: NO
1465
1466
           (vi) ORIGINAL SOURCE:
1467
                 (A) ORGANISM: Lactococcus lactis
1468
           (ix) FEATURE:
1469
1470
                 (A) NAME/KEY: promoter
                 (B) LOCATION:4..60
1471
                 (D) OTHER INFORMATION:/standard name= "Constitutional
1472
1473
                        promoter"
1474
                        /label= Cp7
1475
1476
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
1477
1478
       TATGCGGTAG TTTATTCTTG ACATGACGAG ACAGGTGTGG TATAATGGGT CTAGATTAGG
1479
1480
       60
1481
1482
1483
       (2) INFORMATION FOR SEQ ID NO: 41:
```

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```
(i) SEQUENCE CHARACTERISTICS:
1485
                 (A) LENGTH: 60 base pairs
1486
1487
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
1488
                 (D) TOPOLOGY: linear
1489
1490
           (ii) MOLECULE TYPE: DNA (genomic)
1491
1492
1493
          (iii) HYPOTHETICAL: YES
1494
          (iv) ANTI-SENSE: NO
1495
1496
1497
          (vi) ORIGINAL SOURCE:
                 (A) ORGANISM: Lactococcus lactis
1498
1499
           (ix) FEATURE:
1500
                 (A) NAME/KEY: promoter
1501
                 (B) LOCATION: 4..60
1502
1503
                 (D) OTHER INFORMATION:/standard name= "Constitutional
1504
                        promoter"
                        /label= Cp8
1505
1506
1507
      CATTCTTTAG TTTATTCTTG ACAAACGTAT TGAGGACTGA TATAATAGGT GAGTACTGTT 60
1508
1509
1510
1511
1512
1513
1514
      (2) INFORMATION FOR SEQ ID NO: 42:
1515
           (i) SEQUENCE CHARACTERISTICS:
1516
                 (A) LENGTH: 60 base pairs
1517
                 (B) TYPE: nucleic acid
1518
1519
                 (C) STRANDEDNESS: double
1520
                 (D) TOPOLOGY: linear
1521
1522 (ii) MOLECULE TYPE: DNA (genomic)
          (iii) HYPOTHETICAL: YES
1524
1525
1526
          (iv) ANTI-SENSE: NO
1527
           (vi) ORIGINAL SOURCE:
1528
                 (A) ORGANISM: Lactococcus lactis
1529
1530
           (ix) FEATURE:
1531
                 (A) NAME/KEY: promoter
1532
1533
                 (B) LOCATION:4..60
1534
                 (D) OTHER INFORMATION:/standard_name= "Constitutional
1535
                       promoter"
1536
                        /label= Cp9
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		INPUT SET: \$34081.raw	
	1537		
	1538		
	1539	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:	
	1540	ALLEV .	
	1541	CATAGTCTAG TTTATTCTTG ACACGCGGTC CATTGGCTGG TATAATAATT TAGTACTGTT	
	1542	60 '	
	1543	,	
	1544		
	1545	(2) INFORMATION FOR SEQ ID NO: 43:	
	1546		
	1547	(i) SEQUENCE CHARACTERISTICS:	
>	1548	(A) LENGTH: 177 base pairs	
	1549	(B) TYPE: nucleic acid	
	1550	(C) STRANDEDNESS: double	
	1551	(D) TOPOLOGY: linear	
	1552	(ii) MOVERGIVE BURD DIVE (monomics)	
	1553	(ii) MOLECULE TYPE: DNA (genomic)	
	1554	(iii) whomenerar and	
	1555	(iii) HYPOTHETICAL: YES	
	1556	(iv) ANTI-SENSE: NO	
	1557 1558	(IV) ANII-SENSE: NO	
	1558	(vi) ORIGINAL SOURCE:	
	1560	(A) ORGANISM: Saccharomyces cerevisiae	
	1561	(A) ORGANISM: Saccharomyces cerevisiae	
	1562	(ix) FEATURE:	
	1563	(A) NAME/KEY: promoter	
	1564	(B) LOCATION: 8177	
	1565	(C) IDENTIFICATION METHOD: experimental	
	1566	(D) OTHER INFORMATION:/evidence= EXPERIMENTAL	
	1567	/standard name= "Yeast promoter"	
	1568	/label= Yp102	
	1569	,	
	1570		
	1571	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:	
	1572		
	1573	GAATTCGTGA CTCAAACGGG TGGTCGACGG GTGGTTCCAA TTAATTGGCG TCCCTCTTAT	
	1574	60	
	1575	AAAGGCGAGG GTACGTGCGA CAATTGGTAG AGCGAGCGGG GCTCTTAAGT GCAAGTGACT 120	
	1576	AAAGGCGAGG GTACGTGCGA CAATTGGTAG AGCGAGCGGG GCTCTTAAGT GCAAGTGACT ${}_{\wedge}$ ${}_{\wedge}$ ${}^{\mathcal{N}^{T}}$	
	1577	120	
	1578		
	1579	GCGAACATTT TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC	
	1580	177	
	1581		
	1500	(2) INFORMATION FOR GEO ID NO. 44	
	1582	(2) INFORMATION FOR SEQ ID NO: 44:	
	1583 1584	(i) SEQUENCE CHARACTERISTICS:	
	1584	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 182 base pairs	
	1586	(B) TYPE: nucleic acid	
	1587	(C) STRANDEDNESS: double	
	130/	(C) BITCHIDEDIESS. GOUDIE	

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```
(D) TOPOLOGY: linear
1588
1589
1590
           (ii) MOLECULE TYPE: DNA (genomic)
1591
1592
          (iii) HYPOTHETICAL: YES
1593
1594
           (iv) ANTI-SENSE: NO
1595
1596
           (vi) ORIGINAL SOURCE:
1597
                 (A) ORGANISM: Saccharomyces cerevisiae
1598
           (ix) FEATURE:
1599
1600
                 (A) NAME/KEY: promoter
1601
                 (B) LOCATION:8..181
                 (C) IDENTIFICATION METHOD: experimental
1602
                 (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1603
                        /standard name= "Yeast promoter"
1604
                        /label= Yp112
1605
1606
1607
1608
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
1609
      GAATTCGTGA CTCACGGCAT CTGATGGTTG ACCATAGTCA GGAACATTGT GCTGGAGTTC
1610
1611
1612
1613
      CTTGAGGAAT GAGTTATAAA ATGGGAGGTT GCGGCTAATG CCAGGCAGGA GAGGAACCCT
1614
1615
      CTTAAGTGCA AGTGACTGCA AACATTTTTT TCGTTTGTTG AATCGCTACC AATCATGGAT
1616
1617
1618
1619
      CC
1620
      182
1621
1622 (2) INFORMATION FOR SEQ ID NO: 45:
1623
1624
            (i) SEQUENCE CHARACTERISTICS:
1625
                 (A) LENGTH: 191 base pairs
                 (B) TYPE: nucleic acid
1626
                 (C) STRANDEDNESS: double
1627
1628
                 (D) TOPOLOGY: linear
1629
1630
          (ii) MOLECULE TYPE: DNA (genomic)
1631
          (iii) HYPOTHETICAL: YES
1632
1633
           (iv) ANTI-SENSE: NO
1634
1635
1636
           (vi) ORIGINAL SOURCE:
1637
                 (A) ORGANISM: Saccharomyces cerevisiae
1638
1639
           (ix) FEATURE:
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INPUT SET: S34681.raw
                 (A) NAME/KEY: promoter
1640
1641
                 (B) LOCATION:8..181
1642
                 (C) IDENTIFICATION METHOD: experimental
1643
                 (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
                        /standard name= "Yeast promoter"
1644
1645
                        /label= Yp13
1646
1647
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
1648
1649
1650
       GAATTCGTGA CTCACTAGGC AGGTCACGTT GGCTCTTCGC GGCGCAGGTT CGTATGCCGC
1651
1652
1653
       GCCGCCAGGG GCTTTATAAA GGTCGTCCTG GGTACAGTTG GGATGGCTCC ACGTTTCGGC
1654
1655
       TCTTAAGTGC AAGTGACTGC GAACATTTCG TTTGTTAGAA TAATTCAAGA ATCGCTACCA
1656
1657
1658
1659
      ATCATGGATC C
1660
       191
1661
       (2) INFORMATION FOR SEQ ID NO: 46:
1662
1663
1664
            (i) SEQUENCE CHARACTERISTICS:
1665
                 (A) LENGTH: 167 base pairs
1666
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
1667
1668
                 (D) TOPOLOGY: linear
1669
1670
           (ii) MOLECULE TYPE: DNA (genomic)
1671
1672
          (iii) HYPOTHETICAL: YES
1673
           (iv) ANTI-SENSE: NO
1674
1675
1676
           (vi) ORIGINAL SOURCE:
1677
                 (A) ORGANISM: Saccharomyces cerevisiae
           (ix) FEATURE:
1679
1680
                 (A) NAME/KEY: promoter
                 (B) LOCATION:8..167
1681
                 (C) IDENTIFICATION METHOD: experimental
1682
                 (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1683
                        /standard_name= "Yeast promoter"
1684
                        /label= Yp15
1685
1686
1687
1688
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
1689
1690
      GAATTCGTGA CTCAGGGCCG TACTAAGTAG CTTTCGTATG CTATGCGGGG TTTTATAAAT
1691
```

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```
1692
        CTTTGGGCCA TGGTCTTGCT GGAAAACACC TCTCTTAAGT GCAAGTGACT GCGAACATTT
 1693
 1694
 1695
 1696
        TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC
 1697
 1698
        (2) INFORMATION FOR SEQ ID NO: 47:
 1699
 1700
             (i) SEQUENCE CHARACTERISTICS:
 1701
                  (A) LENGTH: 191 base pairs
 1702
                  (B) TYPE: nucleic acid
 1703
 1704
                  (C) STRANDEDNESS: double
 1705
                  (D) TOPOLOGY: linear
 1706
            (ii) MOLECULE TYPE: DNA (genomic)
. 1707
 1708
           (iii) HYPOTHETICAL: YES
 1709
 1710
            (iv) ANTI-SENSE: NO
 1711
 1712
            (vi) ORIGINAL SOURCE:
 1713
 1714
                  (A) ORGANISM: Saccharomyces cerevisiae
 1715
            (ix) FEATURE:
 1716
                  (A) NAME/KEY: promoter
 1717
                  (B) LOCATION:8..191
 1718
                  (C) IDENTIFICATION METHOD: experimental
 1719
 1720
                  (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
 1721
                         /standard name= "Yeast promoter"
 1722
                         /label= Yp154
 1723
 1724
 1725
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
 1726
 1727
       GAATTCGTGA CTCACCGCTC GGGTGCAGGG CCAAGGCGGC GGAATGTGCG GGGCGTTCTA
 1728
 1729
 1730
       GCGCAATCGG GGTATAAATT TATAAGGAGG CTGCGGGTGC TAGTTTGTCT AGTTTGACTC
 1731
 1732
 1733
       TTAAGTGCAA GTGACTGCGA ACATTTTTCG TTTGTTAGAA TAATTCAAGA ATCGCTACCA
 1734
 1735
       ATCATGGATC C
 1736
 1737
       191
 1738
 1739
        (2) INFORMATION FOR SEQ ID NO: 48:
 1740
 1741
             (i) SEQUENCE CHARACTERISTICS:
 1742
                  (A) LENGTH: 195 base pairs
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```
(B) TYPE: nucleic acid
1743
                 (C) STRANDEDNESS: double
1744
                 (D) TOPOLOGY: linear
1745
1746
1747
           (ii) MOLECULE TYPE: DNA (genomic)
1748
          (iii) HYPOTHETICAL: YES
1749
1750
           (iv) ANTI-SENSE: NO
1751
1752
1753
           (vi) ORIGINAL SOURCE:
1754
                 (A) ORGANISM: Saccharomyces cerevisiae
1755
           (ix) FEATURE:
1756
                 (A) NAME/KEY: promoter
1757
1758
                 (B) LOCATION:8..190
                 (C) IDENTIFICATION METHOD: experimental
1759
                 (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1760
1761
                        /standard name= "Yeast promoter"
1762
                        /label= Yp18
1763
1764
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
1765
1766
      GAATTCGTGA CTCAGGATTA GCTATGCCGG TTGGGATAAG CGAACAACTG GAGGTGAGAA
1767
1768
                                                                              some
1769
1770
      GCTTTTTGTC AGAATATAAA CCCGTTAGTC AGGGTTTGGT GGGATAGGGG GTACTGTACC
1771
1772
1773
      TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT
1774
1775
1776
      ACCAATCATG GATCC
1777
      195
1778
1779
      (2) INFORMATION FOR SEQ ID NO: 49:
1780
            (i) SEQUENCE CHARACTERISTICS:
1781
1782
                 (A) LENGTH: 179 base pairs
1783
                 (B) TYPE: nucleic acid
1784
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear
1785
1786
1787
           (ii) MOLECULE TYPE: DNA (genomic)
1788
1789
          (iii) HYPOTHETICAL: YES
1790
1791
           (iv) ANTI-SENSE: NO
1792
           (vi) ORIGINAL SOURCE:
1793
1794
                 (A) ORGANISM: Saccharomyces cerevisiae
```

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```
1795
           (ix) FEATURE:
1796
1797
                 (A) NAME/KEY: promoter
1798
                 (B) LOCATION:8..179
                 (C) IDENTIFICATION METHOD: experimental
1799
1800
                 (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
                        /standard name= "Yeast promoter"
1801
1802
                        /label= Yp183
1803
1804
1805
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:
1806
1807
       GAATTCGTGA CTCACTAAGG GTTCGCCATT AACAGAATCG CTGGTAGAAC ATCGGTAGTT
1808
1809
       AGGCACCCGA GTATAAACAG GCGGACCCCT CACGGATATC AGCTGATAGT GCGAGCCTCA
1810
1811
1812
      ATGCGAACAT TTTTTTCGTT TGTTAGAATA ATTCAAGAAT CGCTACCAAT CATGGATCC
1813
1814
      179
1815
       (2) INFORMATION FOR SEQ ID NO: 50:
1816
1817
1818
            (i) SEQUENCE CHARACTERISTICS:
1819
                 (A) LENGTH: 195 base pairs
1820
                 (B) TYPE: nucleic acid
1821
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear
1822
1823
1824
           (ii) MOLECULE TYPE: DNA (genomic)
1825
1826
          (iii) HYPOTHETICAL: YES
1827
1828
           (iv) ANTI-SENSE: NO
1829
1830
           (vi) ORIGINAL SOURCE:
1831
                 (A) ORGANISM: Saccharomyces cerevisiae
1832
           (ix) FEATURE:
1833
                 (A) NAME/KEY: promoter
1834
1835
                 (B) LOCATION:8..190
                 (C) IDENTIFICATION METHOD: experimental
1836
1837
                 (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
                        /standard name= "Yest promoter"
1838
1839
                        /label= Yp190
1840
1841
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:
1842
1843
1844
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1845
1846
```

1) . .

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INPUT SET: S34681.raw CGGGTGGTTA CGGCTATAAA TGAGTGTTTG CAGCCGGGTA CGGGCGTACG AGTAGTGATC TCTTAAATGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT ACCAATCATG GATCC (2) INFORMATION FOR SEQ ID NO: 51: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 193 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: YES (iv) ANTI-SENSE: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Saccharomyces cerevisiae (ix) FEATURE: (A) NAME/KEY: promoter (B) LOCATION:8..189 (C) IDENTIFICATION METHOD: experimental (D) OTHER INFORMATION:/evidence= EXPERIMENTAL /standard name= "Yest promoter" /label= Yp191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51: GAATTCGTGA CTCAATGCTG CGGGCGGCAG GAGTCTGGTG TAACTTCCCA TTTTGAGTGA AAGACAGACC ATCTATAAAC ATTTGGTGGG CAAAGTGGCC TGGCGGATTT GTTTGGACTC TTAAGTGAAA GTGACTGCGA ACATTTTTTT CGTTTGTTAG AATAATTCAA GAATCGCTAC CAATCATGGA TCC

1896 (2) INFORMATION FOR SEQ ID NO: 52:

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(i) SEQUENCE CHARACTERISTICS:
1898
                 (A) LENGTH: 166 base pairs
1899
1900
                 (B) TYPE: nucleic acid
1901
                 (C) STRANDEDNESS: double
1902
                 (D) TOPOLOGY: linear
1903
1904
           (ii) MOLECULE TYPE: DNA (genomic)
1905
          (iii) HYPOTHETICAL: YES
1906
1907
           (iv) ANTI-SENSE: NO
1908
1909
1910
           (vi) ORIGINAL SOURCE:
1911
                (A) ORGANISM: Saccharomyces cerevisiae
1912
           (ix) FEATURE:
1913
                 (A) NAME/KEY: promoter
1914
1915
                 (B) LOCATION: 8..166
                 (C) IDENTIFICATION METHOD: experimental
1916
                 (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1917
                        /standard name= "Yeast promoter"
1918
                        /label= Yp192
1919
1920
1921
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:
1922
1923
1924
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1925
1926
      GAAAATTACG ACATTATAAA TAGCGGAGAG GCCAGGTGAT GGGCACCATT GTGGGGGGGC
1927
1928
1929
      TCTTAATTGT TAGAATAATT CAAGAATCGC TACCAATCAT GGATCC
1930
1931
1932
1933
       (2) INFORMATION FOR SEQ ID NO: 53:
1934
1935
            (i) SEQUENCE CHARACTERISTICS:
1936
                 (A) LENGTH: 195 base pairs
1937
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
1938
1939
                 (D) TOPOLOGY: linear
1940
          (ii) MOLECULE TYPE: DNA (genomic)
1941
1942
          (iii) HYPOTHETICAL: YES
1943
1944
          (iv) ANTI-SENSE: NO
1945
1946
1947
           (vi) ORIGINAL SOURCE:
1948
                 (A) ORGANISM: Saccharomyces cerevisiae
1949
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```
(ix) FEATURE:
 1950
                  (A) NAME/KEY: promoter
 1951
 1952
                  (B) LOCATION:8..190
 1953
                  (C) IDENTIFICATION METHOD: experimental
                  (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
 1954
                         /standard_name= "Yeast promoter"
 1955
 1956
                         /label= Yp212
 1957
 1958
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:
 1959
 1960
 1961
       GAATTCGTGA CTCAGTCGCC CGCAAGATGG GATGGTGCAT TTTAAACACC CGAATTATAC
 1962
 1963
 1964
       TCGTCAACTT ATAGTATAAA CGGAACGCGA CGATACGTTC TAGTTTTCGG CGAAGTCGAC
 1965
 1966
       TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT
. 1967
 1968
 1969
 1970
       ACCAATCATG GATCC
 1971
       195
 1972
 1973
        (2) INFORMATION FOR SEQ ID NO: 54:
 1974
 1975
             (i) SEQUENCE CHARACTERISTICS:
 1976
                  (A) LENGTH: 188 base pairs
 1977
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
 1978
 1979
                  (D) TOPOLOGY: linear
 1980
 1981
            (ii) MOLECULE TYPE: DNA (genomic)
 1982
 1983
           (iii) HYPOTHETICAL: YES
 1984
 1985
            (iv) ANTI-SENSE: NO
 1986
 1987
            (vi) ORIGINAL SOURCE:
 1988
                  (A) ORGANISM: Saccharomyces cerevisiae
 1989
 1990
            (ix) FEATURE:
 1991
                  (A) NAME/KEY: promoter
 1992
                  (B) LOCATION:8..183
                  (C) IDENTIFICATION METHOD: experimental
1993
                  (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1994
                         /standard_name= "Yeast promoter"
1995
1996
                         /label= Yp24
1997
 1998
 1999
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:
2000
2001
       GAATTCGTAC TCACGACAGC GTTATGACTT CGAGGACCAG CTACTTCCGG TCGCGTACTA
```

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		INPUT SET: \$34681.raw
	2002	60
	2003	
	2004	GTTTTTACCT GTATAAACTT TGCTACCGCT GGGCCTTGGT GGTGCTGTCC CGCTCTTAAG
	2005	120
	2006	
	2007	TGCAAGTGAC TGCGAACATT TTTTTCGTTT GTTACAATAA TTCAAGAATC GCTACCAATC
	2008	180
	2009	. ι
	2010	ATGGATCC
	2011	188
	2012	
	2012	(2) INFORMATION FOR GEO ID NO. EF.
	2013 2014	(2) INFORMATION FOR SEQ ID NO: 55:
	2014	(i) SEQUENCE CHARACTERISTICS:
>	2015	(A) LENGTH: 195 base pairs
,	2010	(B) TYPE: nucleic acid
	2017	(C) STRANDEDNESS: double
	2018	(D) TOPOLOGY: linear
	2020	(b) Totohoot: Timeat
	2021	(ii) MOLECULE TYPE: DNA (genomic)
	2022	(11) Holdon III. Day (genomic)
	2023	(iii) HYPOTHETICAL: YES
	2024	(===,
	2025	(iv) ANTI-SENSE: NO
	2026	
	2027	(vi) ORIGINAL SOURCE:
	2028	(A) ORGANISM: Saccharomyces cerevisiae
	2029	·
	2030	(ix) FEATURE:
	2031	(A) NAME/KEY: promoter
	2032	(B) LOCATION:8190
	2033	(C) IDENTIFICATION METHOD: experimental
	2034	(D) OTHER INFORMATION:/evidence= EXPERIMENTAL
	2035	/standard_name= "Yeast promoter"
	2036	/label= Yp435
	2037	
	2038	(mil) GROVENIGE PROGREDATON GRO TO NO. 55
	2039	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:
	2040	
	2041	GAATTCGTGA CTAAATGGAT AAGGTTATCG CCATCACGGA GTCTTCTCTC ACGTCTGGAG 60 CAGAGGCTAG ACCTTATAAA TTATACATGG TGGGAGAGGC GATAGTCTTT AGAGACGTGC
	2042 2043	60
	2043	CAGAGGCTAG ACCTTATAAA TTATACATGG TGGGAGAGGC GATAGTCTTT AGAGACGTGC
	2044	120
	2045	120
	2047	TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT
	2047	180
	2049	
	2050	ACCAATCATG GATCC
	2051	195
	2052	

2105

(iv) ANTI-SENSE: NO

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```
2054
                 (i) SEQUENCE CHARACTERISTICS:
     2055
    2056
                      (A) LENGTH: 189 base pairs
-->
     2057
                      (B) TYPE: nucleic acid
     2058
                      (C) STRANDEDNESS: double
     2059
                      (D) TOPOLOGY: linear
     2060
                (ii) MOLECULE TYPE: DNA (genomic)
     2061
     2062
     2063
               (iii) HYPOTHETICAL: YES
     2064
     2065
               (iv) ANTI-SENSE: NO
     2066
     2067
               (vi) ORIGINAL SOURCE:
     2068
                      (A) ORGANISM: Saccharomyces cerevisiae
     2069
     2070
               (ix) FEATURE:
                      (A) NAME/KEY: promoter
     2071
                      (B) LOCATION:8..184
     2072
                      (C) IDENTIFICATION METHOD: experimental
     2073
     2074
                      (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
     2075
                             /standard name= "Yeast promoter"
     2076
                             /label= Yp68
     2077
     2078
     2079
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:
     2080
     2081
           GAATTCGTGA CTCACAAGAA TGTGGGCGGG TCGTTAAACT GAGCCTGGAC ACCTTGGCTG
                                                                                  some
     2082
     2083
     2084
           CGTCGCTTTC GTATAAAGAT CTTAGAGCTG TGGAGTCTGG GTCGAGTGGC CAGCTCTTAA
     2085
     2086
     2087
           ATGCAAGTGA CTGCGAACAT TTTTTTCGTT TGTTAGAATA ATTCAAGAAT CGCTACCAAT
     2088
     2089
     2090
           CATGGATCC
     2091
           189
     2092
     2093 (2) INFORMATION FOR SEQ ID NO: 57:
     2094
     2095
                 (i) SEQUENCE CHARACTERISTICS:
                      (A) LENGTH: 195 base pairs
     2096
                      (B) TYPE: nucleic acid
     2097
     2098
                      (C) STRANDEDNESS: double
     2099
                      (D) TOPOLOGY: linear
     2100
               (ii) MOLECULE TYPE: DNA (genomic)
    2101
     2102
              (iii) HYPOTHETICAL: YES
     2103
     2104
```

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```
2106
           (vi) ORIGINAL SOURCE:
2107
2108
                 (A) ORGANISM: Saccharomyces cerevisiae
2109
2110
           (ix) FEATURE:
2111
                 (A) NAME/KEY: promoter
                 (B) LOCATION:8..190
2112
                 (C) IDENTIFICATION METHOD: experimental
2113
2114
                 (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
2115
                        /standard name= "Yeast promoter"
2116
                        /label= Yp89
2117
2118
2119
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:
2120
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2121
2122
2123
       GGGATTCCCT TCTATATAAA GGGTTCCGAT ACTACGTGCT GCGGACGGCC GATCGAGTTA
2124
2125
2126
2127
       TCTTAAGTGC AAGTGACTGC GAAAATTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT
2128
2129
      ACCAATCATG GATCC
2130
2131
       195
2132
2133
       (2) INFORMATION FOR SEQ ID NO: 58:
2134
2135
            (i) SEQUENCE CHARACTERISTICS:
2136
                 (A) LENGTH: 176 base pairs
2137
                 (B) TYPE: nucleic acid
2138
                 (C) STRANDEDNESS: double
2139
                 (D) TOPOLOGY: linear
2140
2141
          (ii) MOLECULE TYPE: DNA (genomic)
2142
2143
          (iii) HYPOTHETICAL: YES
2144
2145
           (iv) ANTI-SENSE: NO
2146
2147
           (vi) ORIGINAL SOURCE:
2148
                 (A) ORGANISM: Saccharomyces cerevisiae
2149
2150
           (ix) FEATURE:
                 (A) NAME/KEY: promoter
2151
2152
                 (B) LOCATION:8..171
                 (C) IDENTIFICATION METHOD: experimental
2153
                 (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
2154
                        /standard_name= "Yeast promoter"
2155
2156
                        /label= Yp96
2157
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			mar or ser. s	J7001.74W
2158				
2159	(xi) SEQUENCE DES	CRIPTION: SEQ ID NO: 5	8:	
2160	•			
2161	GAATTCGTGA CTCATCTAGT	GAGAGGAGCC GTGGTATCTT	GTGTCACCAC CAGGGGAAAA	A p
2162	60			a nom
2163				/)/0
2164	TAATGGCAGG GGTGTATAAA	TGGTCGAGTA GTCGCGACCC	ACGCTGCAAG GCAAGGAACT	r <i>('</i>
2165	120			
2166				
2167	CTTAAATTTT TTTCGTTTGT	TAGAATAATT CAAGAATCGC	TACCAATCAT GGATCC	
2168	176			
2169				
				•